

REMARKS

This supplemental response was requested by the examiner in a telephone conference on May 21, 2010. As requested, Applicants have amended claims 67, 73, 74, 255, and 278 to clarify the claim language. In this regard, Applicants note that the claims presented herein are amended relative to the claim amendments entered in the response of March 8, 2010. In addition, Applicants have considered the similarity of certain amino acid sequences for the HPIV2 L protein provided by the examiner and present the results of the assessment below. No new matter is added in this response.

Assessment of Amino Acid Sequences Reported for the HPIV2 L Protein:

During the conference call of May 21st, the examiner expressed concern that other HPIV2 protein sequences (GenBank accession numbers NP_598406.1, CAA40788.1, and BAE00056.1) might not have sufficient homology to the sequences disclosed in the application to warrant the scope of the claims. Applicants contend that any such concerns are misplaced.

The sequences corresponding to the accession numbers above were compared via sequence alignment using the default settings of the SIM program of the Expert Protein Analysis System (ExPASY) – available at <http://expasy.org/tools/sim-prot.html>. The sequences for accession numbers NP_598406.1 and CAA40788.1 were found to be 100% identical over their entire 2262 amino acid sequences (the results of this alignment are provided on pages 6-9). Similarly, sequences for accession number BAE00056.1 was found to be 99.3% identical to NP_598406.1 and CAA40788.1, with 15 sequence differences in 2264 amino acids (the results of this alignment are provided on pages 10-13; however, because of the identity of NP_598406.1 and CAA40788.1, the alignment only compares NP_598406.1 with BAE00056.1). Nonetheless, the relevant segments of the sequences for accession numbers NP_598406.1, CAA40788.1, and BAE00056.1 are 100% identical to the HPIV2 L protein amino acid sequences shown in figure 1 of the application.

In comparing the HPIV2 L protein sequences, Applicants noticed that the amino acid numbering of the NP_598406.1 and CAA40788.1 sequences differs slightly from that of BAE00056.1 and figure 1. In particular, residues 948 and 1566 of figure 1 are numbered as

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residues 946 and 1564, respectively, likely due to the presence of residue insertions in the sequence disclosed in the present application. Therefore, Applicants have amended claims 67, 255, and 278 to clarify the scope of the claims. In this regard, the claims now recite residues of the SEQ ID NOs. that correspond to the relevant sequences of figure 1. Applicants note that the claimed SEQ IN NOs. were submitted for the pending application on May 13, 2004. Support for the amended claims can be found throughout the specification, such as in paragraph [39] and figure 1.

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SIM

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Results of SIM with:

Sequence 1: NP_598406 (2362 residues)
Sequence 2: CAA40788.1 (2262 residues)

using the parameters:

Comparison mode: sequences 2
Length of alignment considered: 20
Gap open penalty: -10
Gap extension penalty: 4

 Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet.CH

100.0% identity in 2262 residue overlap; Score: 11957.6; Gap frequency: 0.0%

NP_598406 .	1	M A A S C E L L P E V I N L S P I V K H L I Y V L L G H P P H D L D I R I S M H N D N Q I A R E S C D L
CAA40788.1	1	M A A S C E L L P E V I N L S P I V K H L I Y V L L G H P P H D L D I R I S M H N D N Q I A R E S C D L
<small>*****K*****A*****R*****S*****P*****I*****V*****L*****L*****G*****H*****P*****D*****L*****I*****R*****S*****C*****D*****L*****</small>		
NP_598406 .	61	E R L G V A R G K E L I K V P P E K A T M P G H A V I L N E S C I P P L W K P L P H E K L G P H S O N Y K L I N S
CAA40788.1	61	E R L G V A R G K E L I K V P P E K A T M P G H A V I L N E S C I P P L W K P L P H E K L G P H S O N Y K L I N S
<small>*****E*****R*****G*****V*****A*****R*****G*****K*****E*****L*****I*****K*****V*****P*****P*****E*****K*****A*****T*****M*****P*****E*****K*****A*****T*****M*****P*****E*****K*****G*****H*****P*****S*****G*****H*****P*****K*****L*****G*****P*****H*****E*****K*****L*****I*****N*****S*****</small>		
NP_598406 .	121	C H T I S A I D R C M E I I K L T G H M N L P S R A G I K G I K S I T L M D I Q S I N E S N M Q M A I C
CAA40788.1	121	C H T I S A I D R C M E I I K L T G H M N L P S R E G I G I K G I K S I T L M D I Q S I N E S N M Q M A I C
<small>*****C*****H*****T*****I*****S*****A*****I*****D*****R*****C*****M*****E*****I*****I*****K*****L*****T*****G*****H*****M*****N*****L*****P*****S*****R*****E*****G*****I*****G*****I*****K*****S*****I*****T*****L*****M*****D*****I*****Q*****S*****I*****N*****E*****S*****N*****M*****Q*****M*****A*****I*****C*****</small>		
NP_598406 .	181	I K M I K T E K V M P Q X D M H Q C S Q P T D E P A V N T S R G L V I T N L C P D L N G I V M V P T P G E R T
CAA40788.1	181	I K M I K T E K V M P Q X D M H Q C S Q P T D L V H V D T K S G L V I T N L C P D L N G I V M V P T P G E R T
<small>*****I*****K*****M*****I*****K*****T*****E*****K*****V*****M*****P*****Q*****X*****D*****M*****H*****Q*****C*****S*****Q*****P*****T*****D*****E*****P*****A*****V*****N*****T*****S*****R*****G*****I*****V*****N*****L*****C*****P*****D*****L*****N*****G*****I*****V*****M*****V*****P*****T*****G*****E*****R*****T*****</small>		
NP_598406 .	241	I K M I S M F E Q M N V I T A L C T K S H Y L G E L O P R I D R L F G T V D E L A G Q L G D I V Y K V I A S L E S L V Y
CAA40788.1	241	I K M I S M F E Q M N V I T A L C T K S H Y L G E L O P R I D R L F G T V D E L A G Q L G D I V Y K V I A S L E S L V Y
<small>*****I*****K*****M*****I*****S*****M*****F*****E*****Q*****M*****N*****V*****I*****T*****A*****L*****C*****T*****K*****S*****H*****Y*****L*****G*****E*****L*****O*****P*****R*****I*****D*****R*****L*****F*****G*****T*****V*****D*****E*****L*****A*****G*****Q*****L*****G*****D*****I*****V*****Y*****K*****V*****I*****A*****S*****L*****E*****S*****L*****V*****Y*****</small>		

NP-598406,
CRA49788.1 361 GCLGLKQWVVELEGOSRSRPTIQEKLIDLIGSNGILFPRSTTYTQIQLGIPSNLSWPLIRE
362 GLCQQRDPPVVELANGSPPTDQEITDNLIGSMALYEDSITVTQQLDIZSGJSDLJA

NP-598406,
CRA49788.1 361 MLCUCLURGNGRHTTAAQWNVRENSHCGSKLLQFTIATKLAFFPNTLTIDGTEKKGKNGP
362 MLCUCLURGNGRHTTAAQWVQTCRSGMCAGSKLLDPPFTLNGKLAFFPNTLILTYPERKKKNGP

NP-598406,
CRA49788.1 421 PULIFERASKESTLIEFHODAKISVEYTLKWEKSLIIRPRTCFDFGEEELSPHNAH
421 PULIFERASKESTLIEFHODAKISVEYTLKWEKSLIIRPRTCFDFGEEELSPHNAH

NP-598406,
CRA49788.1 461 SXPREDWNEVFRKLSLQCRQEPHNPINRKLRLLNPLSCDSDFPVAELRYVTHGEYL
461 SXPREDWNEVFRKLSLQCRQEPHNPINRKLRLLNPLSCDSDFPVAELRYVTHGEYL

NP-598406,
CRA49788.1 541 QUDTPCAISLKEKESEIKPDRIFPAKLTNMRSGQVIAEALIANGAGTLMKEMIVVLRQLS
541 QUDTPCAISLKEKESEIKPDRIFPAKLTNMRSGQVIAEALIANGAGTLMKEMIVVLRQLS

NP-598406,
CRA49788.1 601 LTKGILUTMSQIGILSEKAFTTGTDMTSQQPTTIDTSDKMRKSTTAAJSDVLDPLDPLTTEL
601 LTMGLUTMSQIGILSEKAFTTGTDMTSQQPTTIDTSDKMRKSTTAAJSDVLDPLDPLTTEL

NP-598406,
CRA49788.1 661 SACFTTIDDLAKYCLQWRYQTIIIFARTLHMYGVFSLPEDIHLMLIRSTLYVDFPMPFA
661 HACTTIDDLAKYCLQWRYQTIIIFARTLHMYGVFSLPEDIHLMLIRSTLYVDFPMPFA

NP-598406,
CRA49788.1 721 KADAPDALKVLUQDITIVKQZUELLCQWNTWILISVLLSGAENITVNMVYQJUNQA
721 KTAAPDALKVLUQDITIVKQZUELLCQWNTWILISVLLSGAENITVNMVYQJUNQA

NP-598406,
CRA49788.1 781 XAVTTWPRPSLPSTQKKELAYAASKLFFPELRAMNYSLGRHOLYAGETLISSTTFIVSYKV
781 TAUSTRUPPSLPGSIQKKELAYAASKLFFPELRAMNYSLGRHOLKAQBTIIGSTTFIVSYKV

NP-598406,
CRA49788.1 841 FYQGRILTQALKNASKLCLTADVLGETCQASCNSGATTINRLETERGVERDTCVKLNIYQG
841 FYQGRILTQALKNASKLCLTADVLGETCQASCNSGATTINRLETERGVERDTCVKLNIYQG

NP-598406,
CRA49788.1 901 IROLTYELLFPPQYSIPOKTTEIPLZBPKLISKIVLIFSQLGGSLYLAACSPLEPNRMIGLV
901 IROLTYELLFPPQYSIPOKTTEIPLZBPKLISKIVLIFSQLGGSLYLAACSPLEPNRMIGLV

NP-598406,
CRA49788.1 961 LGTAVAHILFRLKFCGALKSNILYNNLLARYFPGNGSWTLLAADPVSQDQEYLPPPTILKRN
962 LGTAVADLRLKFCGALKSNILYNNLLARYFPGNGSWTLLAADPVSQDQEYLPPPTILKRN

NP-598406,
CRA49788.1 1021 TQNTLJARICRFPULRGVPTYNAKKEBELLERKFLIPDILPFBVANLITQOSSIGRNQD
1021 TQNTLJARICRFPULRGVPTYNAKKEBELLERKFLIPDILPFBVANLITQOSSIGRNQD

NP-598406,
CRA49788.1 1081 GPPPTTPTTIPMSAEIKEIESTKKEVSLVKEYSTDVKLEYNYPVILMPLIPSYVNTTQTC

CAAA6788.1 1581 SFFDTTTETIMRPGPEIPLPLSTKTCVLSVIEYNTNTAISYUJFVILQPLPLPFGVLYW LTDQTC

NP-598406 . 1141 SIDITERSLPELGSWSSLNGRTLESLGTETDPIEVVPGFLTVQGNDCCDFC9QGDADCPWTPL
CAA6788.1 1141 SIDITERSLRLSNGSELLNGRTLESLGTETDPIEVVPGFLTVQGNDCCDFC9QGDADCPWTPL

NP-598406 . 1201 FNGTLLDGLPTEPPPIRKPVYIGSGTEREVASRAYTKRGAHSLERALRGAGQVYLMAPGDT
CAA6788.1 1201 FNGTLLDGLPTEPPPIRKPVYIGSGTEREVASRAYTKRGAHSLERALRGAGQVYLMAPGDT

NP-598406 . 1261 VVMMNHALDIANTVXKISLQLQTLTPLTSAMITHKLQDGATLKEPTPAASVAFSYTH
CAA6788.1 1261 VVMMNHALDIANTVXKISLQLQTLTPLTSAMITHKLQDGATLKEPTPAASVAFSYTH

NP-598406 . 1321 ISEDQYALBLIQQRUVLQNLIIYQQLMHTOLAIETTYHNPPIRTESTGSEITLNHNTSSGCCVR
CAA6788.1 1321 ISEDQYALBLIQQRUVLQNLIIYQQLMHTOLAIETTYHNPPIRTESTGSEITLNHNTSSGCCVR

NP-598406 . 1381 SVDDGLCLCESSNGEHPQITVYIETTFVYPPISLADVEIHLADLDSYDACKERSTDYVSLDK
CAA6788.1 1381 SVDDGLCLCESSNGEHPQITVYIETTFVYPPISLADVEIHLADLDSYDACKERSTDYVSLDK

NP-598406 . 1441 TDLLAHLTAKMINSTIGLDETYTIVNAVLSDYTHNNISFCSTKIDLVPKLMANHFL
CAA6788.1 1441 TDLLAHLTAKQIASTIGLDETYTIVNAVLSDYTHNNISFCSTKIDLVPKLMANHFL

UP-598406 . 1501 LELAFQMYVLRISQWINTPLDFTYNTLIRIPNTMLNNIAITSHPKLURRAMELDITTPIN
CAA6788.1 1501 LELAFQMYVLRISQWINTPLDFTYNTLIRIPNTMLNNIAITSHPKLURRAMELDITTPIN

NP-598406 . 1561 APYLAQSLDTVNQLESDGQWGVQVLADLSNGTDELELILSEDMSNETDPMELTAREKTL
CAA6788.1 1561 APYLAQSLDTVNQLESDGQWGVQVLADLSNGTDELELILSEDMSNETDPMELTAREKTL

UP-598406 . 1621 LALUKKGEDVTTFPKTKGMPFEBCCLVLTEYLANCYQGTHLDPDLQKCYLYNUJTMKLTAPF
CAA6788.1 1621 LALUKKGEDVTTFPKTKGMPFEBCCLVLTEYLANCYQGTHLDPDLQKCYLYNUJTMKLTAPF

NP-598406 . 1681 SHNPVLTTRKLIMQIKRSEDQCYLINSYKSTEGQLETDYLILNUTLTAFTYHNEFAGNCWPF
CAA6788.1 1681 SHNPVLTTRKLIMQIKRSEDQCYLINSYKSTEGQLETDYLILNUTLTAFTYHNEFAGNCWPF

NP-598406 . 1741 PFDLFPTP2SLFEPYPLPVONHIFQCSAISTLITGPPSHNVLP10VSETRWYKOLSYCRYLE
CAA6788.1 1741 PFDLFPTP2SLFEPYPLPVONHIFQCSAISTLITGPPSHNVLP10VSETRWYKOLSYCRYLE

NP-598406 . 1801 TQKIQTGDRXIALRSGOASMSELLELIFPGPLTVYTNLSPFSENPPGRNTARLFTQFVQCV
CAA6788.1 1801 TQKIQTGDRXIALRSGOASMSELLELIFPGPLTVYTNLSPFSENPPGRNTARLFTQFVQCV

NP-598406 . 1861 PYELNQJADLANDDNLTIDPVLWNGNGAVTDLOTKDVAFTIHWGARRKAEVRIADEST
CAA6788.1 1861 PYELNQJADLANDDNLTIDPVLWNGNGAVTDLOTKDVAFTIHWGARRKAEVRIADEST

NP-598496 . 1921 ANINQQCTLSRFSQIHSLLIATTVLRERGIGILYNTKEALPFPSRFPSQIAGLLNCFMTJHLIRS
CXA40788.1 1921 ANINQQCTLSRFSQIHSLLIATTVLRERGIGILYNTKEALPFPSRFPSQIAGLLNCFMTJHLIRS

NP-598496 . 1981 SYSDPFRREVYLVCKLRAADFETTNGSALANTFTATLNNNGFTTIRPTVVCSYWQHLENVG
CXA40788.1 1981 SYSDPFRREVYLVCKLRAADFETTNGSALANTFTATLNNNGFTTIRPTVVCSYWQHLENVG

NP-598496 . 2041 KNGKVIDERILDGLATNFFASDNOILRLCGSTTPSSRPMLEIDQLASFDLVQDALUTLITR
CXA40788.1 2041 EKGKVIDERILDGLATNFFASDNOILRLCGSTTPSSRPMLEIDQLASFDLVQDALUTLITR

NP-598496 . 2101 LKEIITKVQGSSTIEDYTTSLLPTPYMTEAAGEVRTTUKILLERSLMNYTYRUMWVLPSSIREK
CXA40788.1 2101 LKEIITKVQGSSTIEDYTTSLLPTPYMTEAAGEVRTTUKILLERSLMNYTYRUMWVLPSSIREK

NP-598496 . 2161 VRQDLELGSPFLMSILSEGTFLKKTITNEGLLDQTRIVISTYFNSHSHVPLMLRPVQNDI
CXA40788.1 2161 VRQDLELGSPFLMSILSEGTFLKKTITNEGLLDQTRIVISTYFNSHSHVPLMLRPVQNDI

NP-598496 . 2221 WKLGSVIYCSETVDIPLIKDQIRETDIFEDIERGIDGEEL
CXA40788.1 2221 WKLGSVIYCSETVDIPLIKDQIRETDIFEDIERGIDGEEL

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Results of SIM with:

Sequence 1: NP_598406.1 (2262 residues)

Sequence 2: BAR00056.1 (2263 residues)

using the parameters:

Comparison method: ALIGNMENT

Number of alignments (computed): 20

Gap open penalty: 10

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH

95.3% identity in 2263 residues overlap; Score: 11637.0; Gap frequency: 0.1%

NP_598406. BAR00056.1	1. MRAGGEIILLPEVHNLSPIVKHLIYLLGKFHDLDLSESTAPLHNNDQDQFREESNL 2. MRASSETLLPEVHNLSPIVKHLIYLLGKFHDLDLSESTAPLHNNDQDQFREESNL
NP_598406. BAR00056.1	61. ERLGWAKSSEILKRYVPPRTRWNRSHAVNLNPSCIPFLVPLPGKLQ/PVVEQNYKLINAS 62. ERLGWAKSSEILKRYVPPRTRWNRSHAVNLNPSCIPFLVPLPGKLQ/PVVEQNYKLINAS
NP_598406. BAR00056.1	121. CTTISDSIDRCMENIISTKLTGNNLFPSRSKGAGWQKMGKJITHRDQSTMEENKQPNVS 121. CTTISDSIDRCMENIISTKLTGNNLFPSRSKGAGWQKMGKJITHRDQSTMEENKQPNVS
NP_598406. BAR00056.1	181. LNL/TIKYQMPQLINHQSGRQPTDLWIIYDTSOLIVITPHELVIQDFDLNSVLMYFPEMT 181. LNL/TIKYQMPQLINHQSGRQPTDLWIIYDTSOLIVITPHELVIQDFDLNSVLMYFPEMT
NP_598406. BAR00056.1	241. LNVSIIMPEGRMIVTALCTISHYLSPGPRIDYLSIVDPLAQQLQDTVIVKVASLGLVY 241. LNVSIIMPEGRMIVTALCTISHYLSPGPRIDYLSIVDPLAQQLQDTVIVKVASLGLVY

NP-598496 . 301 GCLQKXPPVELANPESFITERIPIILIGGVALDYDDESITVTTGQLLDFSNSPULAE
BAE00056 . 1 301 GCLQKADPVYELAMOFHESPIVETIPIILIGGVALDKEGTVTICQALIFMHSFPLAE

NP-598496 . 361 MCLARLNGHFTLTIAQV-GKVREGNCAGKLIDYTTINKTLAFFFHTLNGYRRKKRGMW
BAE00056 . 1 361 MCLCLMLRWGPTLTIAQAGKRVPECNCGKLLDFTTINKTLAFFFHTLNGYRDPFQNMW

NP-598496 . 420 PFLILIPDQASCPPLIEPCHOMAEISIZETLJGKNEELSIEPRKCTDIN9BELSIPMDKA
BAE00056 . 1 421 PFLILIP-KRASYELLETQHDNA651SYVTELCHWKRISLTERPRKCPDMDFJELSLIPFMKDVA

NP-598496 . 480 ISAPRSDMSVFRASLITIQNQRMORHEIIPMPNPNRRLLLMFLEND9PDFVAELRYVWVIEY
BAE00056 . 1 481 LEAPRSDMNGSVPRKGCLIEPQHQRSHITPMNPNFNRELLLNLFLEDSTOFPVAELQVVTISBY

NP-598496 . 540 LQDDITFCASYSLEKEKELEPAGEIPAKLTHRMESCVVIAEAIIAHAGTILMKENGVVNLQ
BAE00056 . 1 541 LQDDITFCASYSLEKEKEIPAKLTHRMESCVVIAEAIIAHAGTILMKENGVVNLQ

NP-598496 . 600 SLTNSL/TMDQEETITRRAKRYTFDMLQSQGPHTTICKTISPKHRRGTTAASYLTD/PDTPE
BAE00056 . 1 601 SLTKESELTMSIGLISSEKARTRYTDRNLISSQGPHTLKTGKMKESITASSYLTD/PDTPE

NP-598496 . 660 LSACPFITPOLAKYCLQWNYQTLIHPARTLNRMYGVPHLPENIKLRLIRNLYZVQDIPRPF
BAE00056 . 1 661 LSACFIFTIDAEYCILQWVQTTIHFARTLNRMYGVPHLPENIKLRLITESTINVQDFNP

NP-598496 . 720 AATDAFDLOCKNLNGQDIIWVE-RSGDLSLQKQNWIMISTGVLLGSHAEKXRMVQHLN
BAE00056 . 1 721 AATDAFDLNNVMMNDIPIFUGPMGNTINGLQCKQNWIMISTEVJILSEAEKTKCMNSVQGDN

NP-598496 . 770 QALAVITRYPELUSIOTKEKELAXAASKLFEGRLRANNYGLGHOLKAGETTILSTPFIYSK
BAE00056 . 1 781 QATATVTRVTSRSLPFGKKELENVRAKSLFPERLRAHUVGLQH/LRSQRTITGSTPFIYK

NP-598496 . 830 RKFVYQGRILTTQALKNAEAKLCLTRDVLGECTQASCMSATTINRLTEGVBERDTCYKLMTY
BAE00056 . 1 841 RKFVYQGRILTTQALKNAEAKLCLTRDVLGECTQASCMSATTINRLTEGVBERDTCYKLMTY

NP-598496 . 890 QSTBQLTYLIFPQSIEGETLSEFLQNPRLYLSRIVLILPSQLCGLAYLACSRILFMRNG
BAE00056 . 1 901 QSTBQLTYLIFPQSIEGETLSEFLQNPRLYLSRIVLILPSQLCGLAYLACSRILFMRNG

NP-598496 . 950 DPLGTAVADLKPLIKCGALESWLIVRLLJARKPGKDECATLIAADPYSLNQBYLYPPTTIK
BAE00056 . 1 961 DPLGTAVADLKPLIKCGALESWLIVRLLJARKPGKDECATLIAADPYSLNQBYLYPPTTIK

NP-598496 . 1010 RPTQNLAEICEMPNLFGVPTONAKKEENLLANPILLEADPVLPRYKMTIYDQSSIGHKKQ
BAE00056 . 1 1021 RPTQNLAEICEMPNLFGVPTONAKKEENLLANPILLEADPVLPRYKMTIYDQSSIGHKKQ

NP-598496 . 1070 TQGFFDTTITRUMRSPRIRPLSTKKTLSVIEZNTRYLSVNNYVILNPLPFGMLZVITUQ

BAR00056.1 1081 IQGFFDTTETPIMRSFSTPLSTKTLVLEYNTRFLSYGIPVILAPLPIFPLVFLVITDQ

NP-598496. 1139 TCGIDISPLRNLMSWSSLNGKRLBGLETPDPTEVNGFLIVTGDCFCRNQGDGCFPTW
BAR00056.1 1141 TCGIDISPLRNLMSWSSLNGKRLBGLETPDPTEVNGFLIVTGDCFCRNQGDGCFPTW

NP-598496. 1199 FLPFMOTITDONGTCMPVIFPVYPIOSRTEERVRASMAITYKEATHSLLKRALQAGSYVINAFO
BAR00056.1 1201 FLPFMGLITIDGDNPTCNPVTPDILNVYPIOSRTEERVRASMAITYKEATHSLLKRALQAGSYVINAFO

NP-598496. 1259 DTIVVNNHMLDTENTRVKEISLEQLGTLLVPLTSRMTIRRLDGEGTTLFPTASSYAFSSY
BAR00056.1 1261 DTIVVNNHMLDTANTWKLSEQLQGTLLFPTSAINTIRRLDGATLTLFPTASSYAFSSY

NP-598496. 1319 THLSNDQQYLTSDQJRVWDNNIITXQJLMTSGLILETTKHFVINTSTQETTMHNTESGCC
BAR00056.1 1321 THLSNDQQYLTSDQJRVWDNNIITXQJLMTSGLILETTKHFVINTSTQETTMHNTESGCC

NP-598496. 1375 VRNEVDCGLCIESQUNEVQIITVFTYTFDPPLADYETABLYTLSYQAKIGSTHYYSLT
BAR00056.1 1381 VRNEVDCGLCIESQHGEVQIITVFTYTFDPPLADYETABLYTLSYQAKIGSTHYYSLT

NP-598496. 1435 DKIPLLNLTKRQMINSLIGLDETVSIWDAVILSDTYTNRNSISBCSYTKILLVFKLMNK
BAR00056.1 1441 DKIPLLNLTKRQMINSLIGLDETVSIWDAVILSDTYTNRNSISBCSYTKILLVFKLMNK

NV-598496. 1499 PPLELAFQNYYLRTSSWTHNIDPYTMWLRKIPGTALENHTLATISHPFLRFAANRLLLITP
BAR00056.1 1501 PPLELAFQNYYLRTSSWTHNIDPYTMWLRKIPGTALENHTLATISHPFLRFAANRLLLITP

NP-598496. 1559 IIAHYPLASLDYWKLSIDAIQWGYKVQVIAALSGNGIOLLELLILSEDGNELSDERMNLLTAKL
BAR00056.1 1561 IIAHYPLASLDYWKLSIDAIQWGYKVQVIAALSGNGIOLLELLILSEDGNELSDERMNLLTAKL

NP-598496. 1619 TLLALWKGNSHTPFLKOMPPEECKVLTEYIPLAMCTQNTNHLMFLQKYLXHLINPMLTA
BAR00056.1 1621 TLLALWKGNSHTPFLKOMPPEECKVLTEYIPLAMCTQNTNHLMFLQKYLXHLINPMLTA

NP-598496. 1679 FPGNNNPyLTKILQIRESDDGQYTITSSYYESFQLETDITLMSTLTAPYNSIISDSESNKVR
BAR00056.1 1681 FPGNNNPyLTKILQIRESDDGQYTITSSYYESFQLETDITLMSTLTAPYNSIISDSESNKVR

NP-598496. 1739 FIFFDIFPPHESLKEYFLPVVDNQGQARLSTLIPGPPSHHVLRFGLGVSSSTAAYKQ1GCRY
BAR00056.1 1741 -LGLDIFPPHESLKEYFLPVVDNQGQARLSTLIPGPPSHHVLRFGLGVSSSTAAYKQ1GCRY

NP-598496. 1799 METQMIQTCGDLVYLRBESGQASLLELLIFPQDITVYVHSLTSSGENPPQRCRTGIFLETQDQVQ
BAR00056.1 1800 LESTEKIQDQHDLYLAESTGQASMLLCLPPQMVVYVNSLPSSEHDPQMRAPLTYTIVQ

NP-598496. 1859 SVPYKLMQADLAID6NLIKDPVFLWROM2BTDLGSTEIDAVAPLHNGAFASTLNHLDL
BAR00056.1 1860 SVPYKLMQADLAID6NLIKDPVFLWROM2BTDLGSTEIDAVAPLHNGAFASTLNHLDL

NP-598406 . 1915 SWRINQQTGLRSQIHLILYLTATTVLKPGQJLILIVKTSEWLPKSPPEQLAGQLLNCFFWKEKILY
BAE00056.1 1920 STANLIEQULERSQIHSLEATTVLVEGCLLYLKIGWLFZFSRPSQASYLNCPTFURILY

NP-598406 . 1979 RSYTSDPESHEVYLVCRLAADPRTTGFSNLLVTTTLHNEGPTTTHPDVVCSTWQHILEN
BAE00056.1 1980 RSYTSDPESHEVYLVCRLAADPRTTGFSNLLVTTTLHNEGPTTTHPDVVCSTWQHILEN

NP-598406 . 2039 YGRVGVKEVIDELDGLATHTFTAGCNTLILRCGGTPGSRKAEIDQLASPDVLVQDALVLTIT
BAE00056.1 2040 YGRVGVKVDETELGLATHTFTAGCNGLILECGTTSRKAEIDQLASPDVLVQDALVLTIT

NP-598406 . 2163 TILKELIEVQOSHSRINTSLLPTEPMYGAAGENKTIILCLLILERSLMYTWRMPLVLPSSTR
BAE00056.1 2165 TILKELITEVQSGHICDTTSLLFTPTYIGEAGKVRTLILERSLMYTWRMPLVLPSSTR

NP-598406 . 2189 DSVPQDLIELGOFSPRMLSLSQTPPLKKEPTYILIDQILTYLSTPPNSHVLNLHRYQK
BAE00056.1 2190 DSVPQDLIELGOFSPRMLSLSQTPPLKNTPKKYLLDQQUARTYVISTPPNSHVLNLHRYQK

NP-598406 . 2219 QIWKALGSVITYCSETVUDPLIKDQIQEDIDNUFDERGIDGEEL
BAE00056.1 2220 QIWKALGSVITYCSETVUDPLIKDQIQEDIDNUFDERGIDGEEL

Supplemental Response at Examiner's Request

Applicants note that this response is being made at the request of the examiner; therefore, no reduction in any patent term extension due to Applicants should occur based on this response (see 37 CFR 1.704(c)(8)).

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